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# Microbial community structure and dynamics during anaerobic digestion of various agricultural waste materials

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## Abstract

The influence of the feedstock type on the microbial communities involved in anaerobic digestion was investigated in laboratory-scale biogas reactors fed with different agricultural waste materials. Community composition and dynamics over 2 months of reactors' operation were investigated by amplicon sequencing and profiling terminal restriction fragment length polymorphisms of 16S rRNA genes. Major bacterial taxa belonged to the Clostridia and Bacteroidetes, whereas the archaeal community was dominated by methanogenic archaea of the orders Methanomicrobiales and Methanosarcinales. Correlation analysis revealed that the community composition was mainly influenced by the feedstock type with the exception of a temperature shift from 38 to 55 °C which caused the most pronounced community shifts. Bacterial communities involved in the anaerobic digestion of conventional substrates such as maize silage combined with cattle manure were relatively stable and similar to each other. In contrast, special waste materials such as chicken manure or Jatropha press cake were digested by very distinct and less diverse communities, indicating partial ammonia inhibition or the influence of other inhibiting factors. Anaerobic digestion of chicken manure relied on syntrophic acetate oxidation as the dominant acetate-consuming process due to the inhibition of aceticlastic methanogenesis. Jatropha as substrate led to the enrichment of fiber-degrading specialists belonging to the genera Actinomyces and Fibrobacter. 

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## Keywords

16S rRNA genes, Biogas, Co-digestion, Pyrosequencing, T-RFLP